

## SEQUENCE LISTING

&lt;110&gt; M&amp;E Biotech A/S

&lt;120&gt; Method for down-regulating GDF-8 activity

&lt;130&gt; AutoVacGDF-8 DK 1

&lt;160&gt; 23

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

Met	Gln	Lys	Leu	Gln	Leu	Cys	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile
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			20					25					30		

Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr
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Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55					60				

Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Val	Ile	Arg	Gln	Leu
65					70					75					80

Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
		100						105					110		

Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu
		115					120					125			

Met	Gln	Val	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
	130					135					140				

Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145					150					155					160

Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
			165						170					175	

Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
		180						185					190		

Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
		195					200					205			

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
 210 215 220  
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
 225 230 235 240  
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys  
 245 250 255  
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
 260 265 270  
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
 275 280 285  
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300  
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
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 Val Asp Arg Cys Gly Cys Ser  
 370 375

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 <213> Meleagris gallopavo

<400> 2  
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 Gln Asn Thr Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu  
 35 40 45  
 Ser Lys Leu Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile  
 50 55 60  
 Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln  
 65 70 75 80  
 Tyr Asp Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp

85					90					95					
Asp	Tyr	His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser
			100					105					110		
Asp	Phe	Leu	Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys
		115					120					125			
Phe	Ser	Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp
	130					135					140				
Ile	Tyr	Leu	Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile
145					150					155					160
Leu	Arg	Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile
				165					170					175	
Arg	Ser	Leu	Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser
			180					185					190		
Ile	Asp	Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser
	195						200					205			
Asn	Leu	Gly	Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu
	210					215					220				
Ala	Val	Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu
225					230					235					240
Glu	Val	Arg	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly
				245					250					255	
Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro
			260					265					270		
Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro
	275						280					285			
Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe
	290					295					300				
Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg
305					310					315					320
Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn
				325					330					335	
Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro
			340					345					350		
Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser						
			355				360								

<210> 3  
 <211> 375  
 <212> PRT

<213> Gallus sp.

<400> 3

Met	Gln	Lys	Leu	Ala	Val	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Gln	Ile	
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Ala	Val	Asp	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn	
			20					25					30			
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
		35					40					45				
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	
65					70					75					80	
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85					90					95		
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
		100						105					110			
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
		115					120					125				
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
			165						170					175		
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
		180						185					190			
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195					200					205				
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Thr	Gly	Arg	Asp	Leu	Ala	Val	Thr	
225					230					235					240	
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	
			245						250					255		
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
		260						265					270			
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300  
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
 340 345 350  
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
 355 360 365  
 Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 4  
 <211> 376  
 <212> PRT  
 <213> Mus musculus

<400> 4  
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 Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu  
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 Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn  
 35 40 45  
 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys  
 50 55 60  
 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln  
 65 70 75 80  
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp  
 85 90 95  
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr  
 100 105 110  
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe  
 115 120 125  
 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
 130 135 140  
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
 145 150 155 160  
 Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg  
 165 170 175

Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser  
180 185 190

Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
195 200 205

Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
210 215 220

Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
225 230 235 240

Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
245 250 255

Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
260 265 270

Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
275 280 285

Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
290 295 300

Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
305 310 315 320

Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
325 330 335

Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
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Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met  
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Val Val Asp Arg Cys Gly Cys Ser  
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<210> 5

<211> 375

<212> PRT

<213> Bos taurus

<400> 5

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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
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Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr  
35 40 45

Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu

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Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu
65					70					75					80
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Leu	Glu	Leu	Ile	Asp	Gln	Phe	Asp	Val
				85					90					95	
Gln	Arg	Asp	Ala	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
			100					105						110	
Ala	Arg	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu
			115				120						125		
Thr	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
			130				135						140		
Lys	Ile	Gln	Tyr	Asn	Lys	Leu	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145				150							155				160
Arg	Pro	Val	Lys	Thr	Pro	Ala	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
				165					170					175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
			180					185					190		
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
			195				200					205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
			210			215					220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
225				230							235				240
Phe	Pro	Glu	Pro	Gly	Glu	Asp	Gly	Leu	Thr	Pro	Phe	Leu	Glu	Val	Lys
				245					250					255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
			260					265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
			275				280					285			
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
			290			295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
305				310							315				320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
				325					330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340					345					350		
Phe	Asn	Gly	Glu	Gly	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val

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 <212> PRT  
 <213> Ovis sp.  
  
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 20                                      25                                      30  
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn  
 35                                      40                                      45  
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
 50                                      55                                      60  
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
 65                                      70                                      75                                      80  
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
 85                                      90                                      95  
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
 100                                      105                                      110  
 Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu  
 115                                      120                                      125  
 Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
 130                                      135                                      140  
 Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
 145                                      150                                      155                                      160  
 Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
 165                                      170                                      175  
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
 180                                      185                                      190  
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
 195                                      200                                      205  
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
 210                                      215                                      220  
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
 225                                      230                                      235                                      240





Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
 130 135 140  
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
 145 150 155 160  
 Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg  
 165 170 175  
 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser  
 180 185 190  
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
 195 200 205  
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
 210 215 220  
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
 225 230 235 240  
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
 245 250 255  
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
 260 265 270  
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 275 280 285  
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
 290 295 300  
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
 305 310 315 320  
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
 325 330 335  
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
 340 345 350  
 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met  
 355 360 365  
 Val Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 8  
 <211> 375  
 <212> PRT  
 <213> Sus scrofa

<400> 8  
 Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile

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Val Ala Gly Pro	Val Asp Leu Asn	Glu Asn Ser Glu Gln	Lys Glu Asn
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Val Glu Lys Glu Gly Leu Cys	Asn Ala Cys Met Trp Arg	Gln Asn Thr	
35	40	45	
Lys Ser Ser Arg Leu Glu Ala Ile	Lys Ile Gln Ile Leu Ser Lys Leu		
50	55	60	
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu			
65	70	75	80
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val			
	85	90	95
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His			
100	105	110	
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu			
115	120	125	
Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser			
130	135	140	
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu			
145	150	155	160
Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu			
	165	170	175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu			
	180	185	190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val			
195	200	205	
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly			
210	215	220	
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr			
225	230	235	240
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys			
	245	250	255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys			
	260	265	270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val			
275	280	285	
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr			
290	295	300	
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys			

305		310		315		320									
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
				325					330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340					345					350		
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
		355						360					365		
Val	Asp	Arg	Cys	Gly	Cys	Ser									
	370					375									

<210> 9  
 <211> 374  
 <212> PRT  
 <213> Danio rerio

<400> 9
Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys
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Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr
20 25 30
Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His
35 40 45
Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys
50 55 60
Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln
65 70 75 80
Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp
85 90 95
Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu
100 105 110
His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro
115 120 125
Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser
130 135 140
Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His
145 150 155 160
Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg
165 170 175
Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys
180 185 190

Ile	Asp	Val	Asn	Ala	Gly	Val	Thr	Ser	Trp	Gln	Ser	Ile	Asp	Val	Lys
	195						200					205			
Gln	Val	Leu	Thr	Val	Trp	Leu	Lys	Gln	Pro	Glu	Thr	Asn	Arg	Gly	Ile
	210					215					220				
Glu	Ile	Asn	Ala	Tyr	Asp	Ala	Lys	Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser
225					230					235					240
Thr	Glu	Thr	Gly	Glu	Asp	Gly	Leu	Leu	Pro	Phe	Met	Glu	Val	Lys	Ile
				245					250					255	
Ser	Glu	Gly	Pro	Lys	Arg	Ile	Arg	Arg	Asp	Ser	Gly	Leu	Asp	Cys	Asp
			260					265					270		
Glu	Asn	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp
	275						280					285			
Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys
290						295					300				
Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Asp	Tyr	Met	Tyr	Leu	Gln	Lys	Tyr
305					310					315					320
Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala	Ser	Pro	Arg	Gly	Thr	Ala	Gly
				325					330					335	
Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe
			340					345					350		
Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ser	Met	Val	Val
		355					360					365			
Asp	Arg	Cys	Gly	Cys	Ser										
	370														

<210> 10  
 <211> 375  
 <212> PRT  
 <213> Papio hamadryas

<400> 10															
Met	Gln	Lys	Leu	Gln	Leu	Cys	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile
1				5					10					15	
Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn
			20					25					30		
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr
		35					40					45			
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55					60				
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu
65					70					75					80

Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	85	90	95
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	100	105	110
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	115	120	125
Met	Gln	Val	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	130	135	140
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	145	150	155
Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	165	170	175
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	180	185	190
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	195	200	205
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	210	215	220
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	225	230	235
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	245	250	255
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	260	265	270
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	275	280	285
Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	290	295	300
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	305	310	315
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	325	330	335
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	340	345	350
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	355	360	365
Val	Asp	Arg	Cys	Gly	Cys	Ser										370	375	

<210> 11  
<211> 109  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)..(109)  
<223> Identical to residues 267-375 in SEQ ID NO: 1

<400> 11  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15  
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30  
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45  
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60  
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80  
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95  
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 12  
<211> 109  
<212> PRT  
<213> Bos taurus

<220>  
<221> PEPTIDE  
<222> (1)..(109)  
<223> Identical to residues 267-375 in SEQ ID NO: 5

<400> 12  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15  
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30  
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45  
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly  
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 13  
<211> 15  
<212> PRT  
<213> Clostridium tetani

<400> 13  
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

<210> 14  
<211> 21  
<212> PRT  
<213> Clostridium tetani

<400> 14  
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15

Ala Ser His Leu Glu  
20

<210> 15  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (18)..(32)  
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
<221> SIMILAR  
<222> (1)..(17)  
<223> Identical to residues 267-283 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (33)..(109)  
<223> Identical to residues 299-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser



<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly  
  
 <400> 15  
 Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
   1                  5                  10                  15  
  
 Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
                   20                  25                  30  
  
 Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
                   35                  40                  45  
  
 Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
   50                  55                  60  
  
 Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
   65                  70                  75                  80  
  
 Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
                   85                  90                  95  
  
 Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
                   100                  105

<210> 16  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (52)..(66)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
 <221> SIMILAR  
 <222> (1)..(51)  
 <223> Identical to residues 267-317 in SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (67)..(109)  
 <223> Identical to residues 333-375 in SEQ ID NO: 1

<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 16

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr  
50 55 60

Glu Leu Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 17

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (83)..(97)

<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>

<221> SIMILAR

<222> (1)..(82)

<223> Identical to residues 267-348 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (98)..(109)

<223> Identical to residues 364-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 17

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys

1	5	10	15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile			
	20	25	30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu			
	35	40	45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala			
	50	55	60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser			
	65	70	75
Pro Ile Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu			
	85	90	95
Leu Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser			
	100	105	

<210> 18  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (21)..(41)  
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> SIMILAR  
 <222> (42)..(109)  
 <223> Identical to residues 307-375 in SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (42)..(109)  
 <223> Identical to residues 308-375 in SEQ ID NO: 1

<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<400> 18			
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys			
1	5	10	15
Arg Tyr Pro Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val			
	20	25	30



Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser
50						55					60				
Ala	Ser	His	Leu	Glu	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
65					70					75					80
Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
				85					90					95	
Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser			
			100					105							

<210> 20  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (79)..(99)  
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> SIMILAR  
 <222> (1)..(78)  
 <223> Identical to residues 267-345 in SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (100)..(109)  
 <223> Identical to residues 366-375 in SEQ ID NO: 1

<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<400> 20  
 Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
 1 5 10 15  
 Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
 20 25 30  
 Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
 35 40 45  
 Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
 50 55 60  
 Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Phe Asn  
 65 70 75 80

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser  
85 90 95

His Leu Glu Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 21  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (84)..(104)  
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> SIMILAR  
<222> (1)..(83)  
<223> Identical to residues 267-349 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (105)..(109)  
<223> Identical to residues 371-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser

<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<400> 21  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro  
85 90 95

Lys Val Ser Ala Ser His Leu Glu Arg Cys Gly Cys Ser  
 100 105

<210> 22  
 <211> 254  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> SIMILAR  
 <222> (110)..(124)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
 <221> SIMILAR  
 <222> (125)..(145)  
 <223> Diphtheria toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> SIMILAR  
 <222> (1)..(109)  
 <223> 109 C-terminal residues of human and bovine GDF-8  
 (residues 267-375 in SEQ ID NO: 1)

<220>  
 <221> SIMILAR  
 <222> (146)..(254)  
 <223> 109 C-terminal residues of human and bovine GDF-8  
 (residues 267-375 in SEQ ID NO: 1)

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<220>  
 <221> SITE  
 <222> (235)..(236)  
 <223> Identical to (90)..(91)

<400> 22  
 Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
 1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
 20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
 35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
 50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
 65 70 75 80

Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
				85					90					95	
Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser	Gln	Tyr	Ile
			100					105					110		
Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Leu	Phe	Asn	Asn	Phe
		115					120					125			
Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu
	130					135					140				
Glu	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys
145					150					155					160
Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp
				165					170					175	
Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys
			180					185					190		
Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln
		195					200					205			
Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met
		210				215					220				
Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr
225					230					235					240
Gly	Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser		
				245					250						

<210> 23  
 <211> 160  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (16)..(36)  
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> MUTAGEN  
 <222> (37)..(51)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
 <221> SIMILAR  
 <222> (1)..(15)  
 <223> Identical to residues 216-230 of SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (52)..(160)



<223> Identical to residues 267-375 of SEQ ID NO: 1

<220>

<221> SITE

<222> (124)

<223> Cys or Ser

<220>

<221> SITE

<222> (141)..(142)

<223> Lys Glu or Glu Gly

<400> 23

Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile	Lys	Ala	Leu	Phe
1				5				10						15	

Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala
			20					25					30		

Ser	His	Leu	Glu	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile
		35					40					45			

Thr	Glu	Leu	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser
	50					55					60				

Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp
65					70					75					80

Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly
				85					90					95	

Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val
			100					105					110		

His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr
		115					120					125			

Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile
	130					135					140				

Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser
145					150					155					160